

AMENDMENTS TO THE CLAIMS:

This listing of claims will replace all prior versions and listings of claims in the application:

1. (Currently Amended) A primer which specifically amplifies *groEL2* gene fragment of *Streptomyces* species comprising the nucleotide sequence of SEQ ID NO: 1, ~~which specifically amplifies *groEL2* gene fragment of *Streptomyces* species.~~
2. (Currently Amended) A primer which specifically amplifies *groEL2* gene fragment of *Streptomyces* species comprising the nucleotide sequence of SEQ ID NO: 2, ~~which specifically amplifies *groEL2* gene fragment of *Streptomyces* species.~~
3. (Currently Amended) A *groEL2* gene fragment derived from *Streptomyces* species or fragment thereof polynucleotide comprising ~~*groEL2* gene fragment derived from *Streptomyces* species or fragment thereof, which is selected from the group consisting of~~ a polynucleotide chosen from the nucleotide sequences of SEQ ID NOs: 3 to 42.
4. (Currently Amended) A polynucleotide *groEL2* gene fragment derived from a potato scab pathogenic microorganism or fragment thereof comprising ~~*groEL2* gene fragment derived from a potato scab pathogenic microorganism or fragment thereof, which is selected from the group consisting of~~ a polynucleotide chosen from the nucleotide sequences of SEQ ID NOs: 43 to 61.
5. (Currently Amended) A method for identifying *Streptomyces* species comprising ~~the steps of:~~

a) amplifying *groEL2* gene fragment of target strain using a primer which is capable of specifically amplifying *groEL2* gene of *Streptomyces* species;
b) analyzing the nucleotide sequence of *groEL2* gene fragment thus amplified;
and
c) comparing the nucleotide sequence obtained in ~~Step-2)~~ b) with that of *groEL2* gene fragment of a reference strain.

6. (Currently Amended) The method of claim 5, wherein the primer is chosen from at least one ~~selected from the group consisting of~~

- a) a primer comprising the nucleotide sequence of SEQ ID NO: 1 and
- b) a primer comprising the nucleotide sequence of SEQ ID NO: 2.

7. (Currently Amended) The method of claim 5, wherein the *groEL2* gene fragment of a reference strain is ~~selected from the group consisting of~~ chosen from the nucleotide sequences of SEQ ID NOs: 3 to 42.

8. (Currently Amended) The method of claim 5, wherein the *groEL2* gene fragment of a reference strain is ~~selected from the group consisting of~~ chosen from the nucleotide sequences of SEQ ID NOs: 43 to 61.

9. (Currently Amended) The method of claim 5, wherein ~~the step-3)~~ c) further comprises ~~the steps of comparing the nucleotide sequence of *groEL2* gene fragment of a target strain with that of a reference strain,~~ multi-aligning the nucleotide sequences, and forming a phylogenetic tree.